

Sequence listing

<110> Kaneka Corporation

<120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237561

<151> 1999-08-24

<160> 2

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

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gagattgagt tcaggacaaa gcttgatcc gtgaggtcta catttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169

Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser

1 5 10

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217

Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser

15 20 25

gca cct tca tta cga cta aga tgt acc ccg acg agc cgg cca tcg agt 265

Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser

30 35 40

tca tgg gct gct gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313

Ser Trp Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp

45 50 55 60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361

Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met

65 70 75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409

Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro

80 85 90

tct ctc gac act gtc gct aaa tac tat gtt cag tct gag gga aag cat 457

Ser	Leu	Asp	Thr	Val	Ala	Lys	Tyr	Tyr	Val	Gln	Ser	Glu	Gly	Lys	His	
95																
att	cgt	ccg	ctc	atg	gta	ctg	ctg	atg	gct	cag	gcg	acg	gag	gtt	gcg	505
Ile	Arg	Pro	Leu	Met	Val	Leu	Leu	Met	Ala	Gln	Ala	Thr	Glu	Val	Ala	
110																
cca	aaa	gtt	cag	ggt	tgg	gag	aag	gtc	gtg	gag	gtt	ccg	gtg	aac	gag	553
Pro	Lys	Val	Gln	Gly	Trp	Glu	Lys	Val	Val	Glu	Val	Pro	Val	Asn	Glu	
125																
gga	ctc	gca	cca	cca	gag	gtg	ctc	aat	gac	aag	aac	cca	gat	atg	atg	601
Gly	Leu	Ala	Pro	Pro	Glu	Val	Leu	Asn	Asp	Lys	Asn	Pro	Asp	Met	Met	
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aac	atg	agg	tca	gga	cca	tta	acg	aag	gac	ggc	gag	atc	gag	gga	cag	649
Asn	Met	Arg	Ser	Gly	Pro	Leu	Thr	Lys	Asp	Gly	Glu	Ile	Glu	Gly	Gln	
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acg	tcg	aat	atc	ctc	gcc	tcg	caa	cg	cg	ttg	gct	gag	atc	acg	gag	697
Thr	Ser	Asn	Ile	Leu	Ala	Ser	Gln	Arg	Arg	Leu	Ala	Glu	Ile	Thr	Glu	
175																
atg	atc	cat	gca	gca	tca	ctc	ctc	cac	gac	gac	gtt	atc	gac	gct	tcc	745
Met	Ile	His	Ala	Ala	Ser	Leu	Leu	His	Asp	Asp	Val	Ile	Asp	Ala	Ser	
190																
gag	acc	aga	cga	aac	gca	cca	tcc	gga	aac	cag	gca	ttc	gga	aac	aag	793
Glu	Thr	Arg	Arg	Asn	Ala	Pro	Ser	Gly	Asn	Gln	Ala	Phe	Gly	Asn	Lys	
205																
atg	gcg	att	ttg	gct	ggt	gat	ttc	ttg	ttg	gga	cg	g	tct	gtt	gca	841
Met	Ala	Ile	Leu	Ala	Gly	Asp	Phe	Leu	Leu	Gly	Arg	Ala	Ser	Val	Ala	
225																
ttg	gcg	agg	ttg	cg	aat	ccg	gag	gt	att	gag	ctt	ttg	gct	act	gtt	889
Leu	Ala	Arg	Leu	Arg	Asn	Pro	Glu	Val	Ile	Glu	Leu	Leu	Ala	Thr	Val	
240																
att	gca	aac	ttg	gtt	gag	gga	gag	ttc	atg	cag	ttg	aaa	aat	act	gtt	937
Ile	Ala	Asn	Leu	Val	Glu	Gly	Glu	Phe	Met	Gln	Leu	Lys	Asn	Thr	Val	
255																
gat	gat	g	att	gag	g	ct	ac	cg	ac	cg	aa	ac	ttc	gat	tac	985
Asp	Asp	Ala	Ile	Glu	Ala	Thr	Ala	Thr	Gln	Glu	Thr	Phe	Asp	Tyr	Tyr	
270																
ttg	cag	aag	act	tac	ttg	aag	act	g	cg	tcc	ttg	att	g	cc	aag	1033

Leu	Gln	Lys	Thr	Tyr	Leu	Lys	Thr	Ala	Ser	Leu	Ile	Ala	Lys	Ser	Cys	
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aga gca agt gcg ctt ctg ggt gct acg cct gag gtt gct gat gct															1081	
Arg	Ala	Ser	Ala	Leu	Leu	Gly	Gly	Ala	Thr	Pro	Glu	Val	Ala	Asp	Ala	
									310					315		
gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac															1129	
Ala	Tyr	Ala	Tyr	Gly	Arg	Asn	Leu	Gly	Leu	Ala	Phe	Gln	Ile	Val	Asp	
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gac atg ctc gac tac acc gtc tcc gct acc gac ctc ggt aag ccc gcc															1177	
Asp	Met	Leu	Asp	Tyr	Thr	Val	Ser	Ala	Thr	Asp	Leu	Gly	Lys	Pro	Ala	
							335		340				345			
ggc gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca															1225	
Gly	Ala	Asp	Leu	Gln	Leu	Gly	Leu	Ala	Thr	Ala	Pro	Ala	Leu	Phe	Ala	
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tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct															1273	
Trp	Lys	His	His	Ala	Glu	Leu	Gly	Pro	Met	Ile	Lys	Arg	Lys	Phe	Ser	
						365		370					375			
gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa aat gat															1321	
Asp	Pro	Gly	Asp	Val	Glu	Arg	Ala	Arg	Glu	Leu	Val	Glu	Lys	Ser	Asp	
						385			390				395			
gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg															1369	
Gly	Leu	Glu	Lys	Thr	Arg	Ala	Leu	Ala	Glu	Glu	Tyr	Ala	Gln	Lys	Ala	
						400		405					410			
ttg gat gca att cgg acg ttc ccg gag agt ccg gca cgg aag gct ttg															1417	
Leu	Asp	Ala	Ile	Arg	Thr	Phe	Pro	Glu	Ser	Pro	Ala	Arg	Lys	Ala	Leu	
						415		420					425			
gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcg agct															1467	
Glu	Gln	Leu	Thr	Asp	Lys	Val	Leu	Thr	Arg	Ser	Arg					
						430		435					440			
cggtaccgg ggatcctcta gagtcgacct gcaggcatgc aagcttggct gtttggcg 1527																
atgagagaag atttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587																
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<210> 2
<211> 440
<212> PRT
<213> Saloella complicata

<400> 2

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							20			25			30	
Ser	Leu	Arg	Leu	Arg	Cys	Thr	Pro	Thr	Ser	Arg	Pro	Ser	Ser	Ser
							35		40			45		
Trp	Ala	Ala	Ala	Val	Ser	Ser	Ala	Ser	Arg	Leu	Val	Glu	Pro	Asp
							50		55			60		
Pro	Asn	Gln	Pro	Leu	Ile	Asn	Pro	Leu	Asn	Leu	Val	Gly	Pro	Glu
							65		70			75		
Met	Ser	Asn	Leu	Thr	Ser	Asn	Ile	Arg	Ser	Leu	Leu	Gly	Ser	Gly
							80		85			90		
His	Pro	Ser	Leu	Asp	Thr	Val	Ala	Lys	Tyr	Tyr	Val	Gln	Ser	Glu
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							110		115			120		
Thr	Glu	Val	Ala	Pro	Lys	Val	Gln	Gly	Trp	Glu	Lys	Val	Val	Glu
							125		130			135		
Val	Pro	Val	Asn	Glu	Gly	Leu	Ala	Pro	Pro	Glu	Val	Leu	Asn	Asp
							140		145			150		
Lys	Asn	Pro	Asp	Met	Met	Asn	Met	Arg	Ser	Gly	Pro	Leu	Thr	Lys
							155		160			165		
Asp	Gly	Glu	Ile	Glu	Gly	Gln	Thr	Ser	Asn	Ile	Leu	Ala	Ser	Gln
							170		175			180		
Arg	Arg	Leu	Ala	Glu	Ile	Thr	Glu	Met	Ile	His	Ala	Ala	Ser	Leu
							185		190			195		
Leu	His	Asp	Asp	Val	Ile	Asp	Ala	Ser	Glu	Thr	Arg	Arg	Asn	Ala
							200		205			210		
Pro	Ser	Gly	Asn	Gln	Ala	Phe	Gly	Asn	Lys	Met	Ala	Ile	Leu	Ala
							215		220			225		
Gly	Asp	Phe	Leu	Leu	Gly	Arg	Ala	Ser	Val	Ala	Leu	Ala	Arg	Leu
							230		235			240		
Arg	Asn	Pro	Glu	Val	Ile	Glu	Leu	Leu	Ala	Thr	Val	Ile	Ala	Asn
							245		250			255		
Leu	Val	Glu	Gly	Glu	Phe	Met	Gln	Leu	Lys	Asn	Thr	Val	Asp	Asp
							260		265			270		
Ala	Ile	Glu	Ala	Thr	Ala	Thr	Gln	Glu	Thr	Phe	Asp	Tyr	Tyr	Leu
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Gln	Lys	Thr	Tyr	Leu	Lys	Thr	Ala	Ser	Leu	Ile	Ala	Lys	Ser	Cys
							290		295			300		
Arg	Ala	Ser	Ala	Leu	Leu	Gly	Gly	Ala	Thr	Pro	Glu	Val	Ala	Asp
							305		310			315		

Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile
320 325 330
Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly
335 340 345
Lys Pro Ala Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro
350 355 360
Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile
365 370 375
Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu
380 385 390
Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala
395 400 405
Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro
410 415 420
Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val
425 430 435
Leu Thr Arg Ser Arg
440